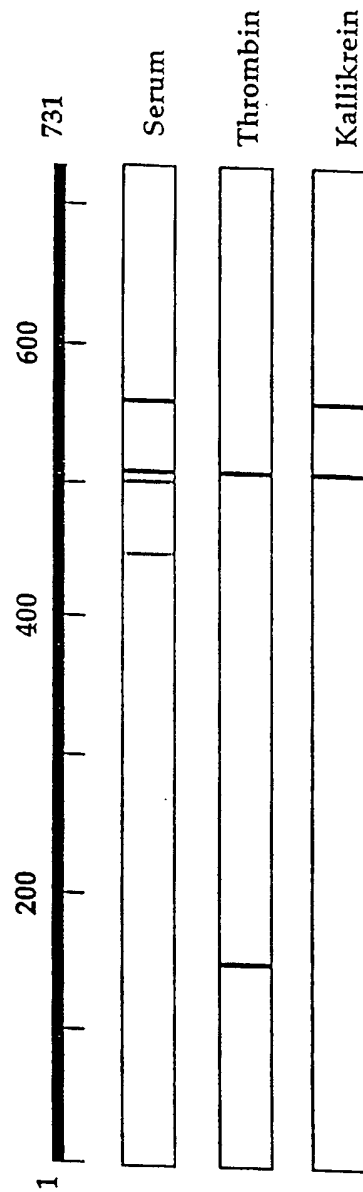Figure 1

```
  1    GATCCATGGGTGGCGTTCCGGGTGCTATCCCGGGTGGCGTTCCGGGTGGTGTATTCTACC    60
       GTACCCACCGCAAGGCCCACGATAGGGCCCACCGCAAGGCCCACCACATAAGATGG

         S   M  G   G   V   P   G   A   I   P   G   G   V   P   G   G   V   F   Y   P
                 ↑
                 Start pf mature processed protein
```

```
 61    CAGGCGCGGGTCTGGGTGCACTGGGCGGTGGTGCGCTGGGCCCGGGTGGTAAACCGCTGA    120
       GTCCGCGCCCAGACCCACGTGACCCGCCACCACGCGACCCGGGCCCACCATTTGGCGACT

         G   A   G   L   G   A   L   G   G   G   A   L   G   P   G   G   K   P   L   K
```

```
121    AACCGGTTCCAGGCGGTCTGGCAGGTGCTGGTCTGGGTGCAGGTCTGGGCGCGTTCCCGG    180
       TTGGCCAAGGTCCGCCAGACCGTCCACGACCAGACCCACGTCCAGACCCGCGCAAGGGCC

         P   V   P   G   G   L   A   G   A   G   L   G   A   G   L   G   A   F   P   A
```

```
181    CGGTTACCTTCCCGGGTGCTCTGGTTCCGGGTGGCGTTGCAGACGCAGCTGCTGCGTACA    240
       GCCAATGGAAGGGCCCACGAGACCAAGGCCCACCGCAACGTCTGCGTCGACGACGCATGT

         V   T   F   P   G   A   L   V   P   G   G   V   A   D   A   A   A   A   Y   K
```

```
241    AAGCGGCAAAGGCAGGTGCGGGTCTGGGCGGGGTACCAGGTGTTGGCGGTCTGGGTGTAT    300
       TTCGCCGTTTCCGTCCACGCCCAGACCCGCCCCATGGTCCACAACCGCCAGACCCACATA

         A   A   K   A   G   A   G   L   G   G   V   P   G   V   G   G   L   G   V   S
```

```
301    CTGCTGGCGCAGTTGTTCCGCAGCCGGGTGCAGGTGTAAAACCGGGCAAAGTTCCAGGTG    360
       GACGACCGCGTCAACAAGGCGTCGGCCCACGTCCACATTTTGGCCCGTTTCAAGGTCCAC

         A   G   A   V   V   P   Q   P   G   A   G   V   K   P   G   K   V   P   G   V
```

```
361    TTGGTCTGCCGGGCGTATACCCGGGTGGTGTTCTGCCGGGCGCGCGTTTCCCAGGTGTTG    420
       AACCAGACGGCCCGCATATGGGCCCACCACAAGACGGCCCGCGCGCAAAGGGTCCACAAC

         G   L   P   G   V   Y   P   G   G   V   L   P   G   A   R   F   P   G   V   G
```

Figure 2(a)

3/26

```
421  GTGTACTGCCGGGCGTTCCGACCGGTGCAGGTGTTAAACCGAAGGCACCAGGTGTAGGCG    480
     CACATGACGGCCCGCAAGGCTGGCCACGTCCACAATTTGGCTTCCGTGGTCCACATCCGC

      V  L  P  G  V  P  T  G  A  G  V  K  P  K  A  P  G  V  G  G
                                           _____
```

```
481  GCGCGTTCGCGGGTATCCCGGGTGTTGGCCCGTTCGGTGGTCCGCAGCCAGGCGTTCCGC    540
     CGCGCAAGCGCCCATAGGGCCCACAACCGGGCAAGCCACCAGGCGTCGGTCCGCAAGGCG

       A  F  A  G  I  P  G  V  G  P  F  G  G  P  Q  P  G  V  P  L
      ____
```

```
541  TGGGTTACCCGATCAAAGCGCCGAAGCTTCCAGGTGGCTACGGTCTGCCGTACACCACCG    600
     ACCCAATGGGCTAGTTTCGCGGCTTCGAAGGTCCACCGATGCCAGACGGCATGTGGTGGC

      G  Y  P  I  K  A  P  K  L  P  G  G  Y  G  L  P  Y  T  T  G
```

```
601  GTAAACTGCCGTACGGCTACGGTCCGGGTGGCGTAGCAGGTGCTGCGGGTAAAGCAGGCT    660
     CATTTGACGGCATGCCGATGCCAGGCCCACCGCATCGTCCACGACGCCCATTTCGTCCGA

      K  L  P  Y  G  Y  G  P  G  G  V  A  G  A  A  G  K  A  G  Y
```

```
661  ACCCAACCGGTACTGGTGTTGGTCCGCAGGCTGCTGCGGCAGCTGCGGCGAAGGCAGCAG    720
     TGGGTTGGCCATGACCACAACCAGGCGTCCGACGACGCCGTCGACGCCGCTTCCGTCGTC

      P  T  G  T  G  V  G  P  Q  A  A  A  A  A  A  A  K  A  A  A
```

```
721  CAAAAATTCGGCGCGGGTGCAGCGGGTGTTCTGCCGGGCGTAGGTGGTGCTGGCGTTCCGG    780
     GTTTTAAGCCGCGCCCACGTCGCCCACAAGACGGCCCGCATCCACCACGACCGCAAGGCC

      K  F  G  A  G  A  A  G  V  L  P  G  V  G  G  A  G  V  P  G
```

```
781  GTGTTCCAGGTGCGATCCCGGGCATCGGTGGTATCGCAGGCGTAGGTACTCCGGCGGCCG    840
     CACAAGGTCCACGCTAGGGCCCGTAGCCACCATAGCGTCCGCATCCATGAGGCCGCCGGC

      V  P  G  A  I  P  G  I  G  G  I  A  G  V  G  T  P  A  A  A
```

```
841  CTGCGGCTGCGGCAGCTGCGGCGAAAGCAGCTAAATACGGTGCGGCAGCAGGCCTGGTTC    900
     GACGCCGACGCCGTCGACGCCGCTTTCGTCGATTTATGCCACGCCGTCGTCCGGACCAAG

      A  A  A  A  A  A  A  K  A  A  K  Y  G  A  A  A  G  L  V  P
```

Figure 2(b)

```
901    CGGGTGGTCCAGGCTTCGGTCCGGGTGTTGTAGGCGTTCCGGGTGCTGGTGTTCCGGGCG    960
       GCCCACCAGGTCCGAAGCCAGGCCCACAACATCCGCAAGGCQCACGACCACAAGGCCCGC

        G  G  P  G  F  G  P  G  V  V  G  V  P  G  A  G  V  P  G  V


961    TAGGTGTTCCAGGTGCGGGCATCCCGGTTGTACCGGGTGCAGGTATCCCGGGCGCTGCGG    1020
       ATCCACAAGGTCCACGCCCGTAGGGCCAACATGGCCCACGTCCATAGGGCCCGCGACGCC

        G  V  P  G  A  G  I  P  V  V  P  G  A  G  I  P  G  A  A  V


1021   TTCCAGGTGTTGTATCCCCGGAAGCGGCAGCTAAGGCTGCTGCGAAAGCTGCGAAATACG    1080
       AAGGTCCACAACATAGGGGCCTTCGCCGTCGATTCCGACGACGCTTTCGACGCTTTATGC

        P  G  V  V  S  P  E  A  A  A  K  A  A  A  K  A  A  K  Y  G


1081   GAGCTCGTCCGGGCGTTGGTGTTGGTGGCATCCCGACCTACGGTGTAGGTGCAGGCGGTT    1140
       CTCGAGCAGGCCCGCAACCACAACCACCGTAGGGCTGGATGCCACATCCACGTCCGCCAA

        A  R  P  G  V  G  V  G  G  I  P  T  Y  G  V  G  A  G  G  F


1141   TCCCAGGTTTCGGCGTTGGTGTTGGTGGCATCCCGGGTGTAGCTGGTGTTCCGTCTGTTG    1200
       AGGGTCCAAAGCCGCAACCACAACCACCGTAGGGCCCACATCGACCACAAGGCAGACAAC

        P  G  F  G  V  G  V  G  G  I  P  G  V  A  G  V  P  S  V  G


1201   GTGGCGTACCGGGTGTTGGTGGCGTTCCAGGTGTAGGTATCTCCCCGGAAGCGCAGGCAG    1260
       CACCGCATGGCCCACAACCACCGCAAGGTCCACATCCATAGAGGGGCCTTCGCGTCCGTC

        G  V  P  G  V  G  G  V  P  G  V  G  I  S  P  E  A  Q  A  A


1261   CTGCGGCAGCTAAAGCAGCGAAGTACGGCGTTGGTACTCCGGCGGCAGCAGCTGCTAAAG    1320
       GACGCCGTCGATTTCGTCGCTTCATGCCGCAACCATGAGGCCGCCGTCGTCGACGATTTC

        A  A  A  K  A  A  K  Y  G  V  G  T  P  A  A  A  A  K  A


1321   CAGCGGCTAAAGCAGCGCAGTTCGGACTAGTTCCGGGCGTAGGTGTTGCGCCAGGTGTTG    1380
       GTCGCCGATTTCGTCGCGTCAAGCCTGATCAAGGCCCGCATCCACAACGCGGTCCACAAC

        A  A  K  A  A  Q  F  G  L  V  P  G  V  G  V  A  P  G  V  G
             ‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾‾
```

Figure 2(c)

1381 GCGTAGCACCGGGTGTTGGTGTTGCTCCGGGCGTAGGTCTGGCACCGGGTGTTGGCGTTG 1440
      CGCATCGTGGCCCACAACCACAACGAGGCCCGCATCCAGACCGTGGCCCACAACCGCAAC

       V   A   P   G   V   G   V   A   P   G   V   G   L   A   P   G   V   G   V   A

1441 CACCAGGTGTAGGTGTTGCGCCGGGCGTTGGTGTAGCACCGGGTATCGGTCCGGGTGGCG 1500
      GTGGTCCACATCCACAACGCGGCCCGCAACCACATCGTGGCCCATAGCCAGGCCCACCGC

       P   G   V   G   V   A   P   G   V   G   V   A   P   G   I   G   P   G   G   V

1501 TTGCGGCTGCTGCGAAATCTGCTGCGAAGGTTGCTGCGAAAGCGCAGCTGCGTGCAGCAG 1560
      AACGCCGACGACGCTTTAGACGACGCTTCCAACGACGCTTTCGCGTCGACGCACGTCGTC

       A   A   A   A   K   S   A   A   K   V   A   A   K   A   Q   L   R   A   A   A
                         _____
                                                               _____

1561 CTGGTCTGGGTGCGGGCATCCCAGGTCTGGGTGTAGGTGTTGGTGTTCCGGGCCTGGGTG 1620
      GACCAGACCCACGCCCGTAGGGTCCAGACCCACATCCACAACCACAAGGCCCGGACCCAC

       G   L   G   A   G   I   P   G   L   G   V   G   V   G   V   P   G   L   G   V
      _____

1621 TAGGTGCAGGGGTACCGGGCCTGGGTGTTGGTGCAGGCGTTCCGGGGTTTCGGTGCTGGCG 1680
      ATCCACGTCCCCATGGCCCGGACCCACAACCACGTCCGCAAGGCCCAAAGCCACGACCGC

       G   A   G   V   P   G   L   G   V   G   A   G   V   P   G   F   G   A   G   A

1681 CGGACGAAGGTGTACGTCGTTCCCTGTCTCCAGAACTGCGTGAAGGTGACCCGTCCTCTT 1740
      GCCTGCTTCCACATGCAGCAAGGGACAGAGGTCTTGACGCACTTCCACTGGGCAGGAGAA

       D   E   G   V   R   R   S   L   S   P   E   L   R   E   G   D   P   S   S   S
                       _____
                           _____

1741 CCCAGCACCTGCCGTCTACCCCGTCCTCTCCACGTGTTCCGGGCGCGCTGGCTGCTGCGA 1800
      GGGTCGTGGACGGCAGATGGGGCAGGAGAGGTGCACAAGGCCCGCGCGACCGACGACGCT

       Q   H   L   P   S   T   P   S   S   P   R   V   P   G   A   L   A   A   A   K
                                                               _____

1801 AAGCGGCGAAATACGGTGCAGCGGTTCCGGGTGTACTGGGCGGTCTGGGTGCTCTGGGCG 1860
      TTCGCCGCTTTATGCCACGTCGCCAAGGCCCACATGACCCGCCAGACCCACGAGACCCGC

       A   A   K   Y   G   A   A   V   P   G   V   L   G   G   L   G   A   L   G   G
      _____

Figure 2(d)

```
1861  GTGTTGGTATCCCGGGCGGTGTTGTAGGTGCAGGCCCAGCTGCAGCTGCTGCTGCGGCAA   1920
      CACAACCATAGGGCCCGCCACAACATCCACGTCCGGGTCGACGTCGACGACGACGCCGTT

       V  G  I  P  G  G  V  V  G  A  G  P  A  A  A  A  A  A  A  K


1921  AGGCAGCGGCGAAAGCAGCTCAGTTCGGTCTGGTTGGTGCAGCAGGTCTGGGCGGTCTGG   1980
      TCCGTCGCCGCTTTCGTCGAGTCAAGCCAGACCAACCACGTCGTCCAGACCCGCCAGACC

       A  A  A  K  A  A  Q  F  G  L  V  G  A  A  G  L  G  G  L  G


1981  GTGTTGGCGGTCTGGGTGTACCGGGCGTTGGTGGTCTGGGTGGCATCCCGCCGGCGGCGG   2040
      CACAACCGCCAGACCCACATGGCCCGCAACCACCAGACCCACCGTAGGGCGGCCGCCGCC

       V  G  G  L  G  V  P  G  V  G  G  L  G  G  I  P  P  A  A  A


2041  CAGCTAAAGCGGCTAAATACGGTGCAGCAGGTCTGGGTGGCGTTCTGGGTGGTGCTGGTC   2100
      GTCGATTTCGCCGATTTATGCCACGTCGTCCAGACCCACCGCAAGACCCACCACGACCAG

       A  K  A  A  K  Y  G  A  A  G  L  G  G  V  L  G  G  A  G  Q


2101  AGTTCCCACTGGGCGGTGTAGCGGCACGTCCGGGTTTCGGTCTGTCCCCGATCTTCCCAG   2160
      TCAAGGGTGACCCGCCACATCGCCGTGCAGGCCCAAAGCCAGACAGGGGCTAGAAGGGTC

       F  P  L  G  G  V  A  A  R  P  G  F  G  L  S  P  I  F  P  G


2161  GCGGTGCATGCCTGGGTAAAGCTTGCGGCCGTAAACGTAAATAATGATAG            2210
      CGCCACGTACGGACCCATTTCGAACGCCGGCATTTGCATTTATTACTATCCTAG
       G   A   C   L   G   K   A   C   G   R   K   R   K   *   *   *
```

Figure 2(e)

```
  1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLG  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 GGVPGAIPGGVPGGVFYPGAGLGALGGGALGPGGKPLKPVPGGLAGAGLG  50

 51 AGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAG 100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 AGLGAFPAVTFPGALVPGGVADAAAAYKAAKAGAGLGGVPGVGGLGVSAG 100

101 AVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 AVVPQPGAGVKPGKVPGVGLPGVYPGGVLPGARFPGVGVLPGVPTGAGVK 150

151 PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 PKAPGVGGAFAGIPGVGPFGGPQPGVPLGYPIKAPKLPGGYGLPYTTGKL 200

201 PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPG 250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 PYGYGPGGVAGAAGKAGYPTGTGVGPQAAAAAAAAKAAAKFGAGAAGVLPG 250

251 VGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGG 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 VGGAGVPGVPGAIPGIGGIAGVGTPAAAAAAAAAAKAAKYGAAAGLVPGG 300

301 PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKA 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 PGFGPGVVGVPGAGVPGVGVPGAGIPVVPGAGIPGAAVPGVVSPEAAAKA 350

351 AAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGV 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 AAKAAKYGARPGVGVGGIPTYGVGAGGFPGFGVGVGGIPGVAGVPSVGGV 400

401 PGVGGVPGVGISPEAQAAAAAAKAAKYGVGTPAAAAAAKAAAKAAQFGLVPG 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 PGVGGVPGVGISPEAQAAAAAAKAAKYGVGTPAAAAAAKAAAKAAQFGLVPG 450

451 VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAA 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPGIGPGGVAA 500

501 AAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAG 550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 AAKSAAKVAAKAQLRAAAGLGAGIPGLGVGVGVPGLGVGAGVPGLGVGAG 550

551 VPGFGAGADEGVRRSLSPELREGDPSSSQHLPSTPSSPRVPGALAAAKAA 600
    ||||||                                  |||||||||||
551 VPGFGA..................................VPGALAAAKAA 567

601 KYGAAVPGVLGGLGALGGVGIPGGVVGAGPARAAAAAAKAAAKAAQFGLVG 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
568 KYGAAVPGVLGGLGALGGVGIPGGVVGAGPARAAAAAAKAAAKAAQFGLVG 617

651 AAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFP 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
618 AAGLGGLGVGGLGVPGVGGLGGIPPAAAAKAAKYGAAGLGGVLGGAGQFP 667

701 LGGVAARPGFGLSPIFPGGACLGKACGRKRK 731
    |||||||||||||||||||||||||||||||
668 LGGVAARPGFGLSPIFPGGACLGKACGRKRK 698
```

Figure 3

```
1   ATGGGTGGCGTTCCGGGTGCTGTTCCGGGTGGCGTTCCGGGTGGTGTATT  50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1   MetGlyGlyValProGlyAlaValProGlyGlyValProGlyGlyValPh  17

51  CTACCCAGGCGCGGGGTTTCGGTGCTGTTCCGGGTGGCGTTGCAGACGCAG  100
    ||||||||||||||||||||||||||||||||||||||||||||||||||
18  eTyrProGlyAlaGlyPheGlyAlaValProGlyGlyValAlaAspAlaA  34

101 CTGCTGCGTACAAAGCGGCAAAGGCAGGTGCGGGTCTGGGCGGGGTACCA  150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
35  laAlaAlaTyrLysAlaAlaLysAlaGlyAlaGlyLeuGlyGlyValPro  50

151 GGTGTTGGCGGTCTGGGTGTATCTGCTGGCGGCAGTTGTTCCGCAGCCGGG  200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
51  GlyValGlyGlyLeuGlyValSerAlaGlyAlaValValProGlnProGl  67

201 TGCAGGTGTAAAACCGGGCAAAGTTCCAGGTGTTGGTCTGCCGGGCGTAT  250
    ||||||||||||||||||||||||||||||||||||||||||||||||||
68  yAlaGlyValLysProGlyLysValProGlyValGlyLeuProGlyValT  84

251 ACCCGGGTTTCGGTGCTGTTCCGGGCGCGCGTTTCCCAGGTGTTGGTGTA  300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
85  yrProGlyPheGlyAlaValProGlyAlaArgPheProGlyValGlyVal  100

301 CTGCCGGGCGTTCCGACCGGTGCAGGTGTTAAAACCGAAGGCACCAGGTGT  350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 LeuProGlyValProThrGlyAlaGlyValLysProLysAlaProGlyVa  117

351 AGGCGGCGCGTTCGCGGGTATCCCGGGTGTTGGCCCGTTCGGTGGTCCGC  400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
118 lGlyGlyAlaPheAlaGlyIleProGlyValGlyProPheGlyGlyProG  134

401 AGCCAGGCGTTCCGCTGGGTTACCCGATCAAAGCGCCGAAGCTTCCAGGT  450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
135 lnProGlyValProLeuGlyTyrProIleLysAlaProLysLeuProGly  150

451 GGCTACGGTCTGCCGTACACCACCGGTAAACTGCCGTACGGCTACGGTCC  500
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 GlyTyrGlyLeuProTyrThrThrGlyLysLeuProTyrGlyTyrGlyPr  167

501 GGGTGGCGTAGCAGGTGCTGCGGGTAAAGCAGGCTACCCAACCGGTACTG  550
    ||||||||||||||||||||||||||||||||||||||||||||||||||
168 oGlyGlyValAlaGlyAlaAlaGlyLysAlaGlyTyrProThrGlyThrG  184

551 GTGTTGGTCCGCAGGCTGCTGCGGCAGCTGCGGCGAAGGCAGCAGCAAAA  600
    ||||||||||||||||||||||||||||||||||||||||||||||||||
185 lyValGlyProGlnAlaAlaAlaAlaAlaAlaAlaAlaLysAlaAlaAlaLys  200

601 TTCGGCGCGGGTGCAGCGGGGTTTCGGTGCTGTTCCGGGGCGTAGGTGGTGC  650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 PheGlyAlaGlyAlaAlaGlyPheGlyAlaValProGlyValGlyGlyAl  217

651 TGGCCGTTCCGGGTGTTCCAGGTGCGATCCCGGGCATCGGTGGTATCGCAG  700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
218 aGlyValProGlyValProGlyAlaIleProGlyIleGlyGlyIleAlaG  234

701 GCGTAGGTACTCCGGCGGCCGCTGCGGCTGCGGCAGCTGCGGCGAAAGCA  750
    ||||||||||||||||||||||||||||||||||||||||||||||||||
235 lyValGlyThrProAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaLysAla  250

751 GCTAAATACGGTGCGGCAGCAGGCCTGGTTCCGGGTGGTCCAGGCTTCGG  800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 AlaLysTyrGlyAlaAlaAlaGlyLeuValProGlyGlyProGlyPheGl  267

801 TCCGGGTGTTGTAGGCCGTTCCGGGTTTCGGTGCTGTTCCGGGCGTAGGTG  850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
```

Figure 4(a)

```
268 yProGlyValValGlyValProGlyPheGlyAlaValProGlyValGlyV 284

851 TTCCAGGTGCGGGCATCCCGGTTGTACCGGGTGCAGGTATCCCGGGCGCT 900
    ||||||||||||||||||||||||||||||||||||||||||||||||||
285 alProGlyAlaGlyIleProValValProGlyAlaGlyIleProGlyAla 300

901 GCGGGTTTCGGTGCTGTATCCCCGGAAGCGGCAGCTAAGGCTGCTGCGAA 950
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 AlaGlyPheGlyAlaValSerProGluAlaAlaAlaLysAlaAlaAlaLy 317

951 AGCTGCGAAATACGGAGCTCGTCCGGGCGTTGGTGTTGGTGGCATCCCGA 1000
    |||||-|-|||||||||||||||||||||||||||||||||||||||||||
318 sAlaAlaLysTyrGlyAlaArgProGlyValGlyValGlyGlyIleProT 334

1001 CCTACGGTGTAGGTGCAGGCGGTTTCCCAGGTTTCGGCGTTGGTGTTGGT 1050
     |||||||||||||||||||||||||||||||||||||||||||||||||||
335 hrTyrGlyValGlyAlaGlyGlyPheProGlyPheGlyValGlyValGly 350

1051 GGCATCCCGGGTGTGTAGCTGGTGTTCCGTCTGTTGGTGGCGTACCGGGTGT 1100
     ||||||||||||||||||||||||||||||||||||||||||||||||||
351 GlyIleProGlyValAlaGlyValProSerValGlyGlyValProGlyVa 367

1101 TGGTGGCGTTCCAGGTGTAGGTATCTCCCCGGAAGCGCAGGCAGCTGCGG 1150
     ||||||||||||||||||||||||||||||||||||||||||||||||||
368 lGlyGlyValProGlyValGlyIleSerProGluAlaGlnAlaAlaAlaA 384

1151 CAGCTAAAGCAGCGAAGTACGGCGTTGGTACTCCGGCGGCAGCAGCTGCT 1200
     ||||||||||||||||||||||||||||||||||||||||||||||||||
385 laAlaLysAlaAlaLysTyrGlyValGlyThrProAlaAlaAlaAlaAla 400

1201 AAAGCAGCGGCTAAAGCAGCGCAGTTCGGACTAGTTCCGGGCGTAGGTGT 1250
     ||||||||||||||||||||||||||||||||||||||||||||||||||
401 LysAlaAlaAlaLysAlaAlaGlnPheGlyLeuValProGlyValGlyVa 417

1251 TGCGCCAGGTGTTGGCGTAGCACCGGGTGTGTTGGTGTTGCTCCGGGCGTAG 1300
     ||||||||||||||||||||||||||||||||||||||||||||||||||
418 lAlaProGlyValGlyValAlaProGlyValGlyValAlaProGlyValG 434

1301 GTCTGGCACCGGGTGTTGGCGTTGCACCAGGTGTAGGTGTTGCGCCGGGC 1350
     ||||||||||||||||||||||||||||||||||||||||||||||||||
435 lyLeuAlaProGlyValGlyValAlaProGlyValGlyValAlaProGly 450

1351 GTTGGTGTAGCACCGGGTATCGGTCCGGGTGGCGTTGCGGCTGCTGCGAA 1400
     ||||||||||||||||||||||||||||||||||||||||||||||||||
451 ValGlyValAlaProGlyIleGlyProGlyGlyValAlaAlaAlaAlaLy 467

1401 ATCTGCTGCGAAGGTTGCTGCGAAAGCGCAGCTGCGTGCAGCAGCTGGTC 1450
     ||||||||||||||||||||||||||||||||||||||||||||||||||
468 sSerAlaAlaLysValAlaAlaLysAlaGlnLeuArgAlaAlaAlaGlyL 484

1451 TGGGTGCGGGCATCCCAGGTCTGGGTGTAGGTGTTGGTGTTCCGGGCCTG 1500
     ||||||||||||||||||||||||||||||||||||||||||||||||||
485 euGlyAlaGlyIleProGlyLeuGlyValGlyValGlyValProGlyLeu 500

1501 GGTGTAGGTGCAGGGGTACCGGGCCTGGGTGTTGGTGCAGGCGTTCCGGG 1550
     ||||||||||||||||||||||||||||||||||||||||||||||||||
501 GlyValGlyAlaGlyValProGlyLeuGlyValGlyAlaGlyValProGl 517

1551 TTTCGGTGCTGTTCCGGGCGCGCTGGCTGCTGCGAAAGCGGCGAAATACG 1600
     ||||||||||||||||||||||||||||||||||||||||||||||||||
518 yPheGlyAlaValProGlyAlaLeuAlaAlaAlaLysAlaAlaLysTyrG 534

1601 GTGCTGTTCCGGGTGTGTACTGGGCGGTCTGGGTGCTCTGGGCGGTGTTGGT 1650
     ||||||||||||||||||||||||||||||||||||||||||||||||||
535 lyAlaValProGlyValLeuGlyGlyLeuGlyAlaLeuGlyGlyValGly 550

1651 ATCCCGGGCGGTGTTGTAGGTGCAGGCCCAGCTGCAGCTGCTGCTGCGGC 170C
     ||||||||||||||||||||||||||||||||||||||||||||||||||
551 IleProGlyGlyValValGlyAlaGlyProAlaAlaAlaAlaAlaAlaAl 567
```

Figure 4(b)

```
1701 AAAGGCAGCGGCGAAAGCAGCTCAGTTCGGTCTGGTTGGTGCAGCAGGTC 1750
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 568 aLysAlaAlaAlaLysAlaAlaGlnPheGlyLeuValGlyAlaAlaGlyL 584

1751 TGGGCGGTCTGGGTGTTGGCGGTCTGGGTGTACCGGGCGTTGGTGGTCTG 1800
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 585 euGlyGlyLeuGlyValGlyGlyLeuGlyValProGlyValGlyGlyLeu 600

1801 GGTGGCATCCCGCCGGCGGCGGCAGCTAAAGCGGCTAAATACGGTGCAGC 1850
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 601 GlyGlyIleProProAlaAlaAlaAlaLysAlaAlaLysTyrGlyAlaAl 617

1851 AGGTCTGGGTGGCGTTCTGGGTGGTGCTGGTCAGTTCCCACTGGGCGGTG 1900
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 618 aGlyLeuGlyGlyValLeuGlyGlyAlaGlyGlnPheProLeuGlyGlyV 634

1901 TAGCGGCACGTCCGGGGTTTCGGTCTGTCCCGGATCTTCCCAGGCGGTGCA 1950
     ||||||||||||||||||||||||||||||||||||||||||||||||||
 635 alAlaAlaArgProGlyPheGlyLeuSerProIlePheProGlyGlyAla 650

1951 TGCCTGGGTAAAGCTTGCGGCCGTAAACGTAAA 1983
     |||||||||||||||||||||||||||||||||
 651 CysLeuGlyLysAlaCysGlyArgLysArgLys 661
```

Figure 4(c)

Figure 5

12/26

Figure 6

Figure 7

Figure 8

Figure 9

Figure 10

Figure 11

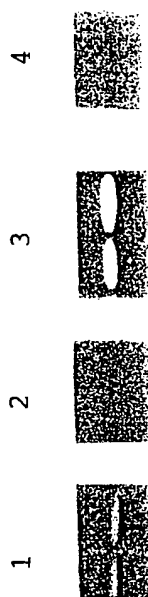Figure 12

Figure 13

Figure 14
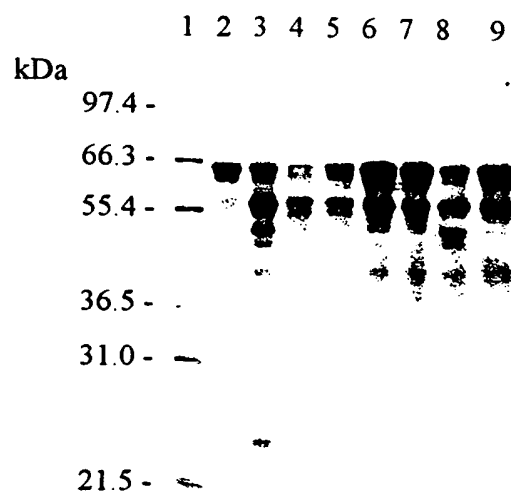
Figure 15

22/26

Figure 16

Figure 17

24/26

Figure 18

Figure 19

Figure 20